
<120> Novel STRA6 Polypeptides

150 - 67-197089
151 - 2000-C4-14

01500 60 228914
01511 2000-08-29

..170.. FastSEQ for Windows Version 4.0

- (220)•
- (221)• CDS
- (222)• (49) ... (2052)

[illegible]

295

300

305

tac cag gtg gcc ctg ctg ctg ctg gtg ggc gtg gta ccc act atc cag 1017
 Tyr Gln Val Ala Leu Leu Leu Leu Val Gly Val Val Pro Thr Ile Gln
 310 315 320

aag gtg agg gca ggg gtc acc acg gat gtc tcc tac ctg ctg gcc ggc 1065
 Lys Val Arg Ala Gly Val Thr Thr Asp Val Ser Tyr Leu Leu Ala Gly
 325 330 335

ttt gga atc gtg ctg tcc gag gac aag cag gag gtg gtg gag ctg gtg 1115
 Phe Gly Ile Val Leu Ser Glu Asp Lys Gln Glu Val Val Glu Leu Val
 340 345 350 355

aag cac cat ctg tgg gct ctg gaa gtg tgc tac atc tca gcc ttg gtc 1161
 Lys His His Leu Trp Ala Leu Glu Val Cys Tyr Ile Ser Ala Leu Val
 360 365 370

ttg tcc tgc tta ctg acc ttc ctg gtc ctg atg cgc tca ctg gtg aca 1209
 Leu Ser Cys Leu Leu Thr Phe Leu Val Leu Met Arg Ser Leu Val Thr
 375 380 385

cac agg acc aac ctt cga gct ctg cac cga gga gct gcc ctg gac ttg 1257
 His Arg Thr Asn Leu Arg Ala Leu His Arg Gly Ala Ala Leu Asp Leu
 390 395 400

agt ccc ttg cat cgg agt ccc cat ccc tcc cgc caa gcc ata ttc tgt 1305
 Ser Pro Leu His Arg Ser Pro His Pro Ser Arg Gln Ala Ile Phe Cys
 405 410 415

tgg atg agc ttc agt gcc tac cag aca gcc ttt atc tgc ctt ggg ctg 1353
 Trp Met Ser Phe Ser Ala Tyr Gln Thr Ala Phe Ile Cys Leu Gly Leu
 420 425 430 435

ctg gtg cag cag atc atc ttc ttc ctg gga acc acg gcc ctg gcc ttc 1401
 Leu Val Gln Gln Ile Ile Phe Phe Leu Gly Thr Thr Ala Leu Ala Phe
 440 445 450

ctg tgg ctg atc atc gtc ctg ctg ctg ctg ctg ctg ctg ctg ctg ctg 1449
 Leu Val Leu Met Ile Val Leu His Gly Arg Asn Leu Leu Ile Ile Arg
 455 460 465

ctg tgg ctg atc atc gtc ctg ctg ctg ctg ctg ctg ctg ctg ctg ctg 1497
 Ser Leu Gln Ser Ser Trp Pro Ile Trp Leu Thr Leu Ala Leu Ala Val
 470 475 480

atc ctg cag aac atc gca gcc cat tgg ctg tcc ctg gag acc cat gat 1545
 Ile Leu Gln Asn Met Ala Ala His Trp Val Phe Leu Glu Thr His Asp
 485 490 495

ctg tgg ctg atc atc gtc ctg ctg ctg ctg ctg ctg ctg ctg ctg ctg
 Leu Val Leu Met Ile Val Leu His Gly Arg Asn Leu Leu Ile Ile Arg

aga gtg ctc ctc tct gcc ctc tac aac gcc atc cac ctt ggc cag atg 1099
Arg Val Leu Leu Ser Ala Leu Tyr Asn Ala Ile His Leu Gly Gln Met
535 540 545

Tac Aag Taa Cga Aac Ttg Ttg Aag Att Gaa Gtc Agc Cag Tcg Cgt Cca 1745
Tyr Thr Tyr Arg Asn Phe Leu Lys Ile Glu Val Ser Gln Ser His Pro
565 570 575

ccc agg acc atg gca gcc ccc cag gac agc ctc aga cca ggg gag gaa 1881
 Pro Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro Gly Glu Glu
 600 605 610

gct agg ccc ggg gcc agc cgc ggc agg gct cgc tgg ggt ctg gcc tac 1977
Ala Arg Pro Gly Ala Ser Arg Gly Arg Ala Arg Trp Gly Leu Ala Tyr
630 635 640

ttg ggt gcr aat ggt gcc cag ccc tga gggcagggaa ggtaaccca 2072
 Leu Gly Ala Asn Gly Ala Gln Pro *
 660 665

<220>

<221> CDS

<222> (186)...(2160)

<400> 4

cacacaccagc caccctctctt ggatccaccagc ccagctgggtg ctgggctcag aggagaagggc 60
cccggtgttgg gagcaccctg ctggcttggg gggacaaagt tccgggagag atcaataaag 120
gaaaggaag agacaaggaa gggagaggtc aggagagcgc ctgattggag gagaaggggc 180
agaga atg tgg tcc cag cca gca ggg aac cag acc tcc ccc ggg ggc aca 240
Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr
1 5 10 15

gag gac tac tcc tat ggc agc tgg tac atc gat gag ccc cag ggg ggc 270
Glu Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly
20 25 30

gag gag ctg cag cca gag ggg gaa gtg ccc tcc tgc cac acc agc ata 320
Glu Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile
35 40 45

cca ccc ggc ctg tac cac gcc tgc ctg gcc tgg ctg tca atc ctt gtg 374
Pro Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val
50 55 60

ctg ctg ctg ctg gcc atg ctg gtg agg cgc cgc cag ctg tgg cct gac 422
Leu Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp
65 70 75

tgt gtg cgt ggc agg ccc ggc ctg ccc agg ccc cgg gca gtg cct gct 470
Cys Val Arg Gly Arg Pro Gly Leu Pro Arg Pro Arg Ala Val Pro Ala
80 85 90 95

gct gtt ttc atg gtc ctg ctg agc tcc ctg tgt ttg ctg ctg ccc gac 518
Ala Val Phe Met Val Leu Leu Ser Ser Leu Cys Leu Leu Leu Pro Asp
100 105 110

gag gac gca ttg ccc ttc ctg act ctg gcc tca gca ccc agc caa gat 566
Glu Asp Ala Leu Pro Phe Leu Thr Leu Ala Ser Ala Pro Ser Gln Asp
115 120 125

ttt aat ggt tat tct cca att ttt ggt ttt aat ata ctg gtt ctt ttt 618
Phe Lys Thr Ala Ala Phe Arg Gly Ala Thr Lys Ile Leu Gly Leu Ile
130 135 140

tat tat ggt gac ctg tac tac cct ctg gct gct tgt gac agc att ggt 666
Tyr Tyr Ala Ala Leu Tyr Tyr Pro Leu Ala Ala Cys Ala Thr Ala Gly
145 150 155

tac aca ggt tca gac ttg gtt ggt ggt ggt ggt ggt ggt ggt ggt ggt 714
Tyr Lys Thr Ala Ala Phe Arg Gly Ala Thr Lys Ile Leu Gly Leu Ile
160 165 170

Tyr Lys Tyr Tyr Ser Leu Leu Ala Ser Leu Pro Leu Leu Leu Gly Leu
195 200 205

gga ttc ctg agc att tgg tac cct gtg cag ctg gtg aga agc ttc agc 204
Gly Phe Leu Ser Leu Trp Tyr Pro Val Gln Leu Val Arg Ser Phe Ser
210 215 220

agt agg aca gga gaa ggc tcc aag ggg ctg cag agc agc tac tct gag 202
Arg Arg Thr Gly Ala Gly Ser Lys Gly Leu Gln Ser Ser Tyr Ser Glu
225 230 235

gaa tat ctg agg aac ctc att tgc agg aag aag ctg gga agc agc tac 250
Glu Tyr Leu Arg Asn Leu Leu Cys Arg Lys Lys Leu Gly Ser Ser Tyr
240 245 250 255

cac acc tcc aag cat ggc ttc ctg tcc tgg gcc cgc gtc tgc ttg aga 998
His Thr Ser Lys His Gly Phe Leu Ser Trp Ala Arg Val Cys Leu Arg
260 265 270

cac tgc atc tac act cca cag cca gga ttc cat ctc ccg ctg aag ctg 1046
His Cys Ile Tyr Thr Pro Gln Pro Gly Phe His Leu Pro Leu Lys Leu
275 280 285

gtg att tca gct aca ctg aca ggg acg gcc att tac cag gtg gcc ctg 1094
Val Leu Ser Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu
290 295 300

ctg ctg ctg gtg ggc gtg gta ccc act atc cag aag gtg agg gca ggg 1142
Leu Leu Leu Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly
305 310 315

gtc acc acg gat gtc tcc tac ctg ctg gcc ggc ttt gga atc gtg ctc 1190
Val Thr Thr Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu
320 325 330 335

tcc gag gac aag cag gag gtg gtg gag ctg gtg aag cag cat ctg tgg 1238
Ser Glu Asp Lys Gln Glu Val Val Glu Leu Val Lys His His Leu Trp
340 345 350

gga ttc gga gga gga gga gga gga gga gga gga gga gga gga gga gga 1280
Ala Leu Val Val Tyr Tyr Ile Ser Ala Leu Val Leu Ser Tyr Leu Leu
355 360 365 370 375 380 385 390 395 400

acc ttc ctg gtc ctg atc agc tca ctg gtg aca cag agc aca aac att 1324
Thr Phe Leu Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu
395 400 405 410 415 420 425 430 435 440

gga ttc gga gga gga gga gga gga gga gga gga gga gga gga gga gga 1368
Ala Leu Val Val Tyr Tyr Ile Ser Ala Leu Val Leu Ser Tyr Leu Leu
445 450 455 460 465 470 475 480 485 490 495 500

gga ttc gga gga gga gga gga gga gga gga gga gga gga gga gga gga 1412
Ala Leu Val Val Tyr Tyr Ile Ser Ala Leu Val Leu Ser Tyr Leu Leu
505 510 515 520 525 530 535 540 545 550 555 560

420

425

430

atc ttc ttc ctg gga acc acg gcc ctg gcc ttc ctg gtg ctg atg cct 1816
 Ile Phe Phe Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro
 435 440 445

gtg ctg cat gga agg aac ctg ctg ctg ttc cgt tcc ctg gag tcc tgg 1824
 Val Leu His Gly Arg Asn Leu Leu Leu Phe Arg Ser Leu Glu Ser Ser
 450 455 460

tgg ccc ttc tgg ctg act ttg gcc ctg got gtg atc ctg cag aac atg 1622
 Trp Pro Phe Trp Leu Thr Leu Ala Leu Ala Val Ile Leu Gln Asn Met
 465 470 475

gca gcc cat tgg gtc ttc ctg gag act cat gat gga cac cca cag ctg 1670
 Ala Ala His Trp Val Phe Leu Gln Thr His Asp Gly His Pro Gln Leu
 480 485 490 495

acc aac cgg cga gtg ctg tat gca gcc acc ttt ctt ctg ttc ccc ctg 1718
 Thr Asn Arg Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu
 500 505 510

aat gtg ctg gtg ggt gcc ata gtg gcc acc tgg cga gtg ctg ctg tot 1766
 Asn Val Leu Val Gly Ala Ile Val Ala Thr Trp Arg Val Leu Leu Ser
 515 520 525

gcc ctg tac aac gcc atc cac ctt ggc cag atg gac ctg agc ctg ctg 1814
 Ala Leu Tyr Asn Ala Ile His Leu Gly Gln Met Asp Leu Ser Leu Leu
 530 535 540

cca ccg aga gcc gcc act ctg gac ccc ggc tac tac acg tac cga aac 1862
 Pro Pro Arg Ala Ala Thr Leu Asp Pro Gly Tyr Tyr Thr Tyr Arg Asn
 545 550 555

ttc ttg aag att gaa gtc agc cag tgg cat cca gcc atg aca gcc ttc 1910
 Phe Leu Lys Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe
 560 565 570 575

tgc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 1962
 Tyr Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

ala pro gln asp ser leu arg pro gly glu glu asp glu gly met gln 1962
 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

ctg cta tgc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 1962
 Leu Leu Val Thr Lys Asp Ser Met Ala Lys Gly Ala Arg Ile Gly Ala
 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

ala pro gln asp ser leu arg pro gly glu glu asp glu gly met gln 1962
 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

gac caa ttt gaggagagg gaggtaacc caactgccc tetgtgtja
Ala Gln Pro

2211

ggcatgtt tggctaccac ctctctccctc cccggtcttc ctcccagcat cacaccagcc 2260
atgcagccag gaggctctcc ggatcactgt ggttgggtgg aggtctgtot gaactgggag 2320
ctccaggagg gctctgtctc acccaacttg ctatgggaga gccagcaggg gttctggaga 2380
agaaactt tgggttaggg ccttgggtcca ggagccagtt gagccagggc agccacatcc 2440
aggttttt tgggttaggg ccttgggtcca ggagccagtt gagccagggc agccacatcc 2500
ggaaactt tgggttaggg ccttgggtcca ggagccagtt gagccagggc agccacatcc 2560
gaactctc tgggttaggg ccttgggtcca ggagccagtt gagccagggc agccacatcc 2620
gaactctc tgggttaggg ccttgggtcca ggagccagtt gagccagggc agccacatcc 2680
cacactggg agccagatat tttgtagt ttatgctt tgctattat gaaagaggtt 2740
aggtgttt tgggttaggg ccttgggtcca ggagccagtt gagccagggc agccacatcc 2800

0210 - E

0211 - GSe

0212 - FRT

0213 - Homo sapiens

0400 - E

Met	Ser	Ser	Gln	Pro	Ala	Gly	Asn	Gln	Thr	Ser	Pro	Gly	Ala	Thr	Glu
1			5					10					15		
Asp	Tyr	Ser	Tyr	Gly	Ser	Trp	Tyr	Ile	Asp	Glu	Pro	Gln	Gly	Gly	Glu
	20						25					30			
Gln	Leu	Gln	Pro	Gln	Gly	Glu	Val	Pro	Ser	Cys	His	Thr	Ser	Ile	Pro
	35					40					45				
Pro	Gly	Leu	Tyr	His	Ala	Cys	Leu	Ala	Ser	Leu	Ser	Ile	Leu	Val	Leu
	50					55				60					
Leu	Leu	Leu	Ala	Met	Leu	Val	Arg	Arg	Arg	Gln	Leu	Trp	Pro	Asp	Cys
	65				70				75					80	
Val	Arg	Gly	Arg	Pro	Gly	Leu	Pro	Arg	Pro	Arg	Ala	Val	Pro	Ala	Ala
	85						90					95			
Val	Phe	Met	Val	Leu	Leu	Ser	Ser	Leu	Cys	Leu	Leu	Leu	Pro	Asp	Glu
	100						105					110			
Asp	Ala	Leu	Ile	Phe	Leu	Thr	Leu	Ala	Ser	Ala	Pro	Ser	Gln	Asp	Gly
	115					120						125			
Lys	Thr	Ala	Ala	Phe	Ala	Gly	Ala	Trp	Lys	Ile	Leu	Gly	Leu	Ile	Tyr
	130					135					140				
Tyr	Ala	Ala	Leu	Tyr	Tyr	Ile	Leu	Ala	Ala	Cys	Ala	Thr	Ala	Gly	His
	145					150				155				160	
Thr	Ala	Leu	His	Leu	Leu	Gly	Ser	Thr	Leu	Ser	Trp	Ala	His	Leu	Gly
	165					170				175				180	
Val	Gln	Val	Trp	Gln	Arg	Ala	Glu	Cys	Pro	Gln	Val	Pro	Lys	Ile	Tyr
	185					190				195				200	
Lys	Tyr	Tyr	Ser	Leu	Leu	Ala	Ser	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Gly
	205					210				215				220	
Ile	Leu	Ser	Leu	Ile	Tyr	Ile	Val	Gln	Leu	Val	Arg	Ser	Ile	Ser	Arg

0400 - E
0401 - GSe
0402 - FRT
0403 - Homo sapiens

278	280	285
Leu Ser Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu Leu		
290	295	300
Leu Leu Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly Val		
305	310	315
Thr Thr Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu Ser		
	325	330
		335
Glu Asp Lys Gln Glu Val Val Glu Leu Val Lys His His Leu Trp Ala		
	340	345
		350
Leu Glu Val Lys Tyr Ile Ser Ala Leu Val Leu Ser Cys Leu Leu Thr		
	355	360
		365
Phe Leu Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu Arg		
	370	375
		380
Ala Leu His Arg Gly Ala Ala Leu Asp Leu Ser Pro Leu His Arg Ser		
	385	390
		395
Pro His Pro Ser Arg Gln Ala Ile Phe Cys Trp Met Ser Phe Ser Ala		
	405	410
		415
Tyr Gln Thr Ala Phe Ile Cys Leu Gly Leu Leu Val Gln Gln Ile Ile		
	420	425
		430
Phe Phe Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro Val		
	435	440
		445
Leu His Gly Arg Asn Leu Leu Leu Phe Arg Ser Leu Glu Ser Ser Trp		
	450	455
		460
Pro Phe Trp Leu Thr Leu Ala Leu Ala Val Ile Leu Gln Asn Met Ala		
	465	470
		475
Ala His Trp Val Phe Leu Glu Thr His Asp Gly His Pro Gln Leu Thr		
	485	490
		495
Asn Arg Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn		
	500	505
		510
Val Leu Val Gly Ala Ile Val Ala Thr Trp Arg Val Leu Leu Ser Ala		
	515	520
		525
Leu Tyr Asn Ala Ile His Leu Gly Gln Met Asp Leu Ser Leu Leu Pro		
	530	535
		540
Pro Arg Ala Ala Thr Leu Asp Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe		
	545	550
		555
Leu Lys Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe Cys		
	565	570
		575
Ser Leu Leu Leu Gln Ala Gln Ser Leu Leu Pro Arg Thr Met Ala Ala		
	580	585
		590
Phe Asn Asp Ser Leu Arg Phe Gly Thr Val Asp Ala Gly Met Gln Leu		
	595	600
		605
Leu Gln Thr Lys Arg Ser Met Ala Lys Gly Ala Arg Phe Gly Asn Ser		
	610	615
		620
Arg Gly Arg Ala Arg Trp Gly Leu Ala Tyr Thr Leu Leu His Asn Pro		
	625	630
		635
Thr Leu Val Val Phe Arg Lys Thr Ala Leu Leu Gly Ala Asn Gly Ala		
	640	645
		650

Ala Phe